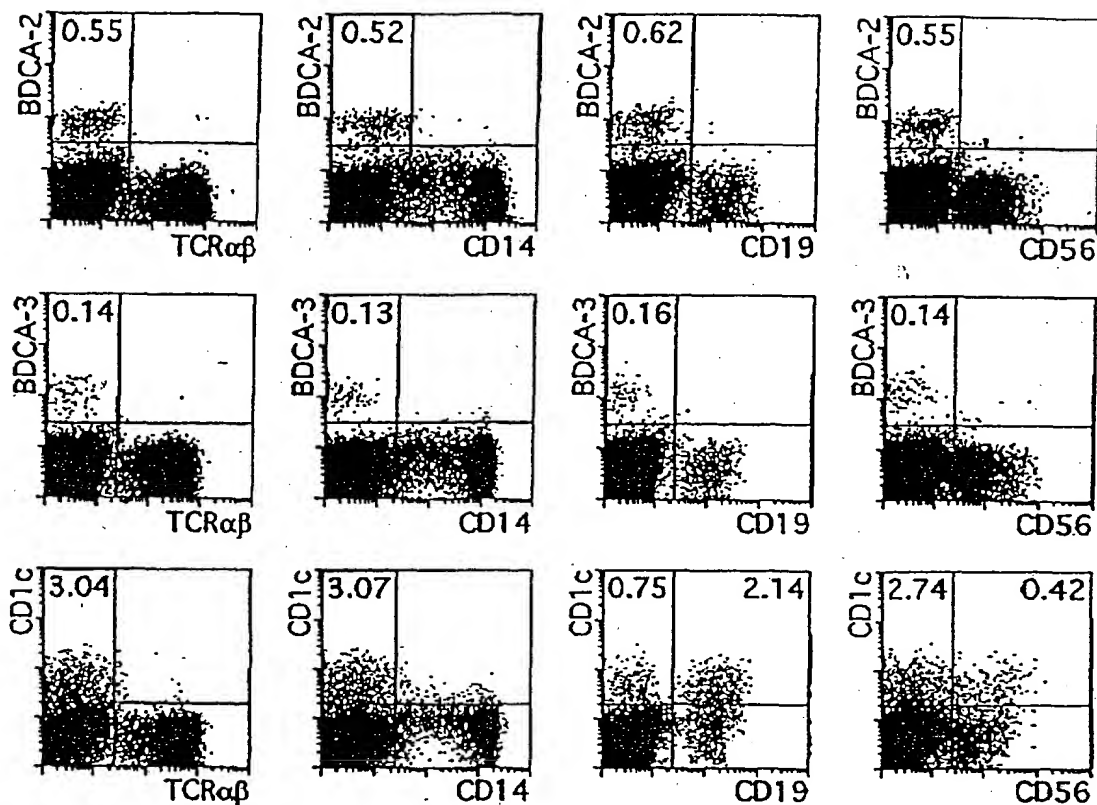


FIGURE 1

A



B

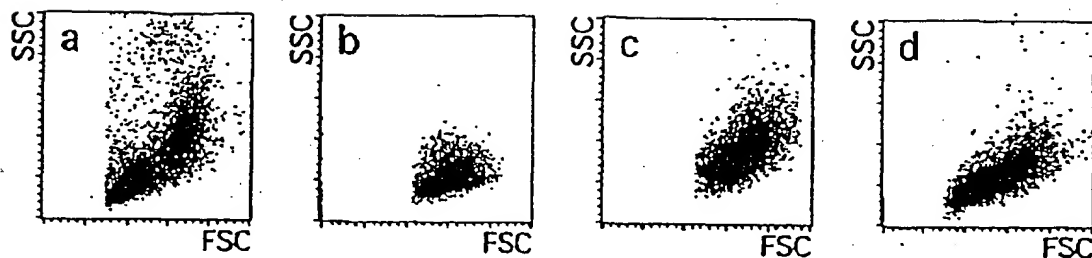


FIGURE 2

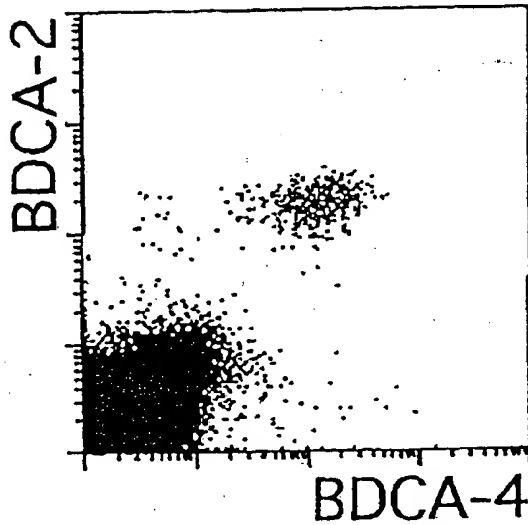


FIGURE 3

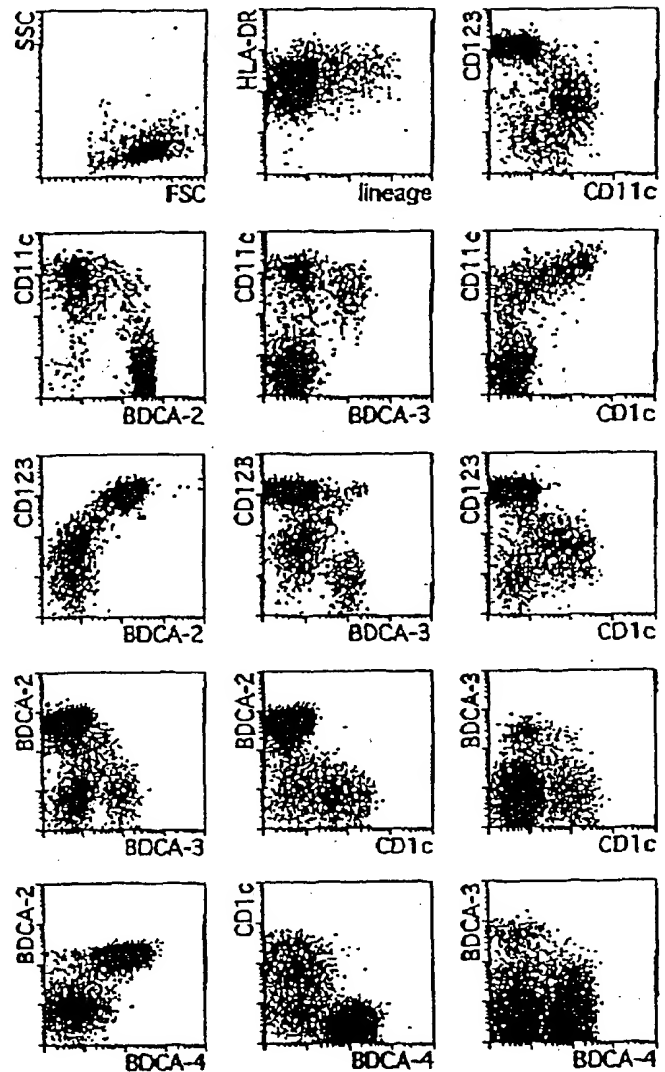
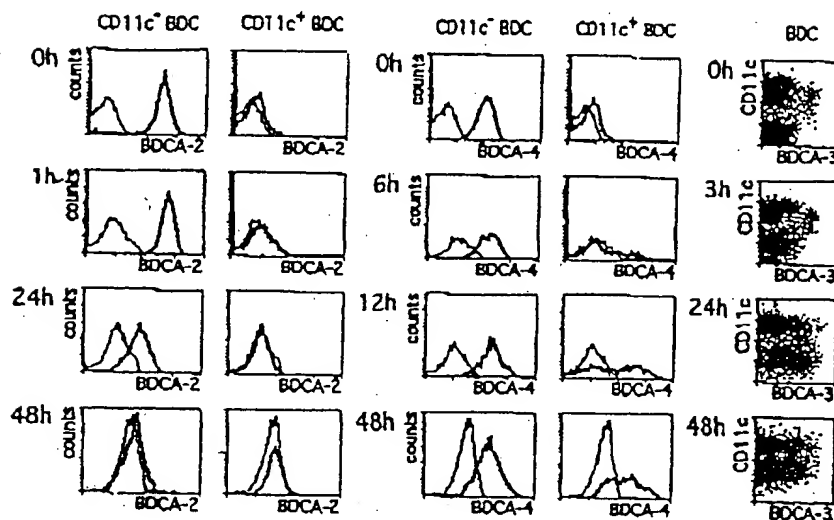


FIGURE 4

A



B

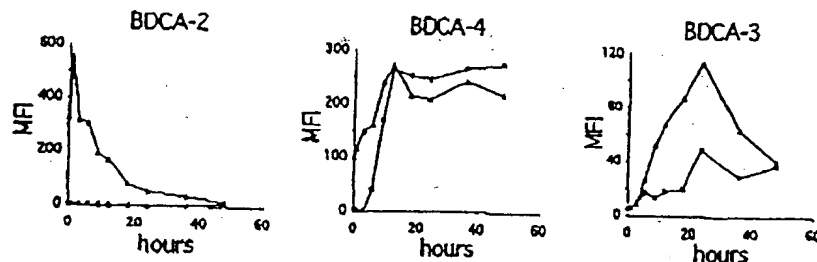


FIGURE 5

MVPEEPPQDREKGLWWFQLKVWSMAVVSILLLSVCFTVSSVVPHNFMYS
 KTVKRLSKLREYQQYHPSLTCVMEGKDIEDWSCCPTPWTSFQSSCYFISTG
 MQSWTKSQKNCSVMGADLVVINTREEQDFIIQNLRNSSFYFLGLSDPGGR
 RHWQWVDQTPYNENVTFWHSGEPPNNLDERCAIINFRSSEEWGWNDIHCH
 VPQKSICKMKKIYI (SEQ ID NO:2)



FIGURE 6

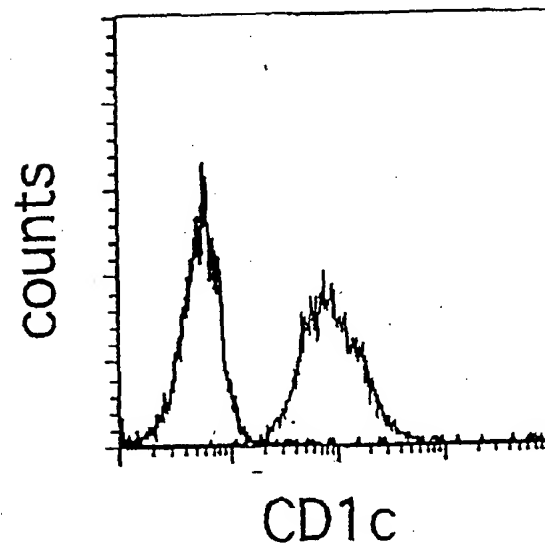


FIGURE 7

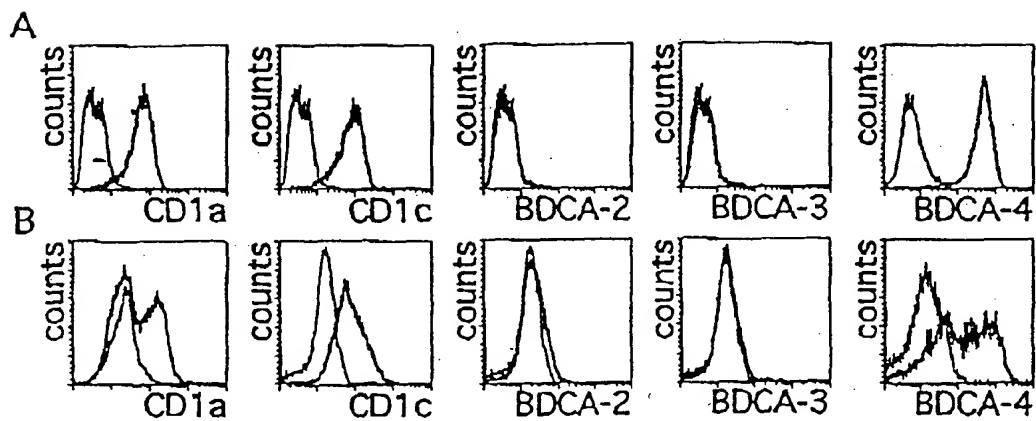


FIGURE 8

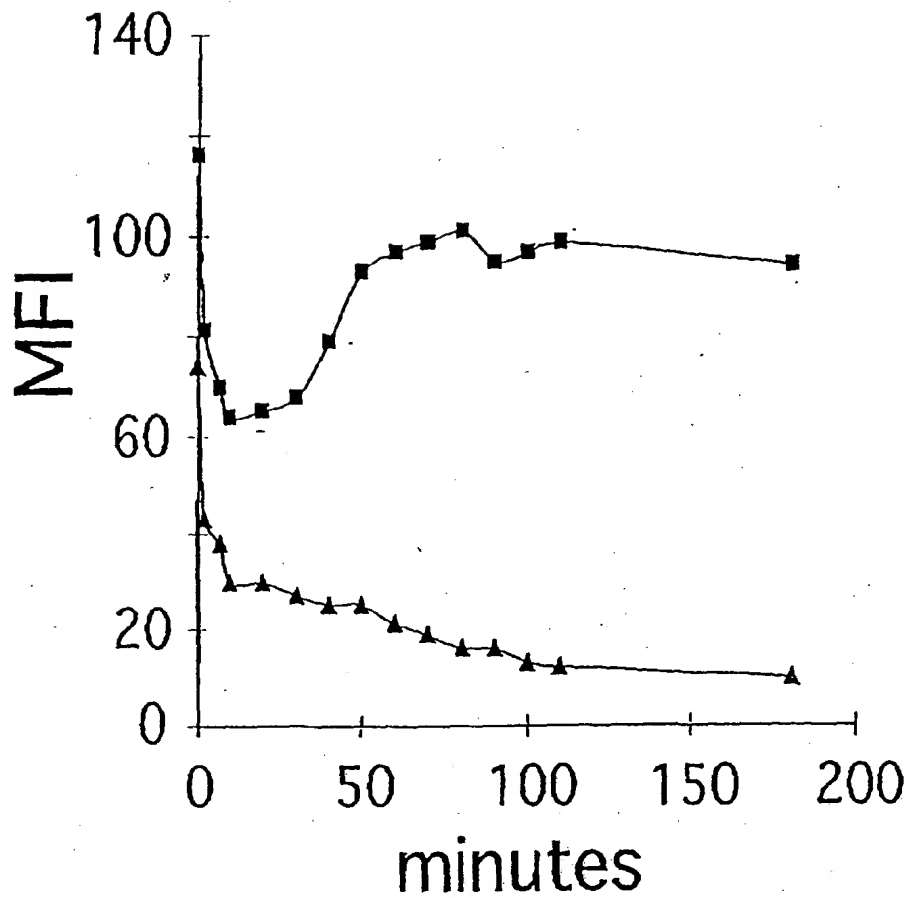


FIGURE 9

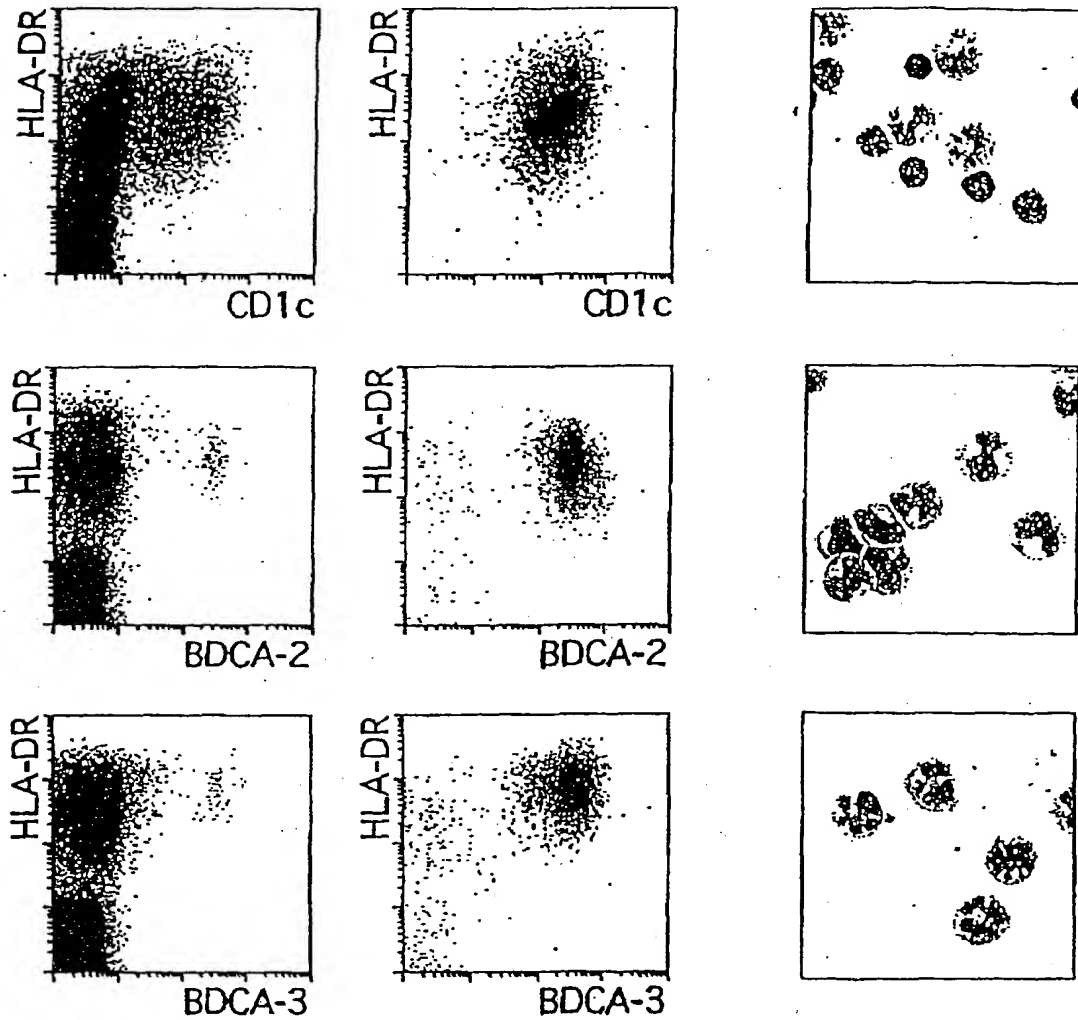


FIGURE 10

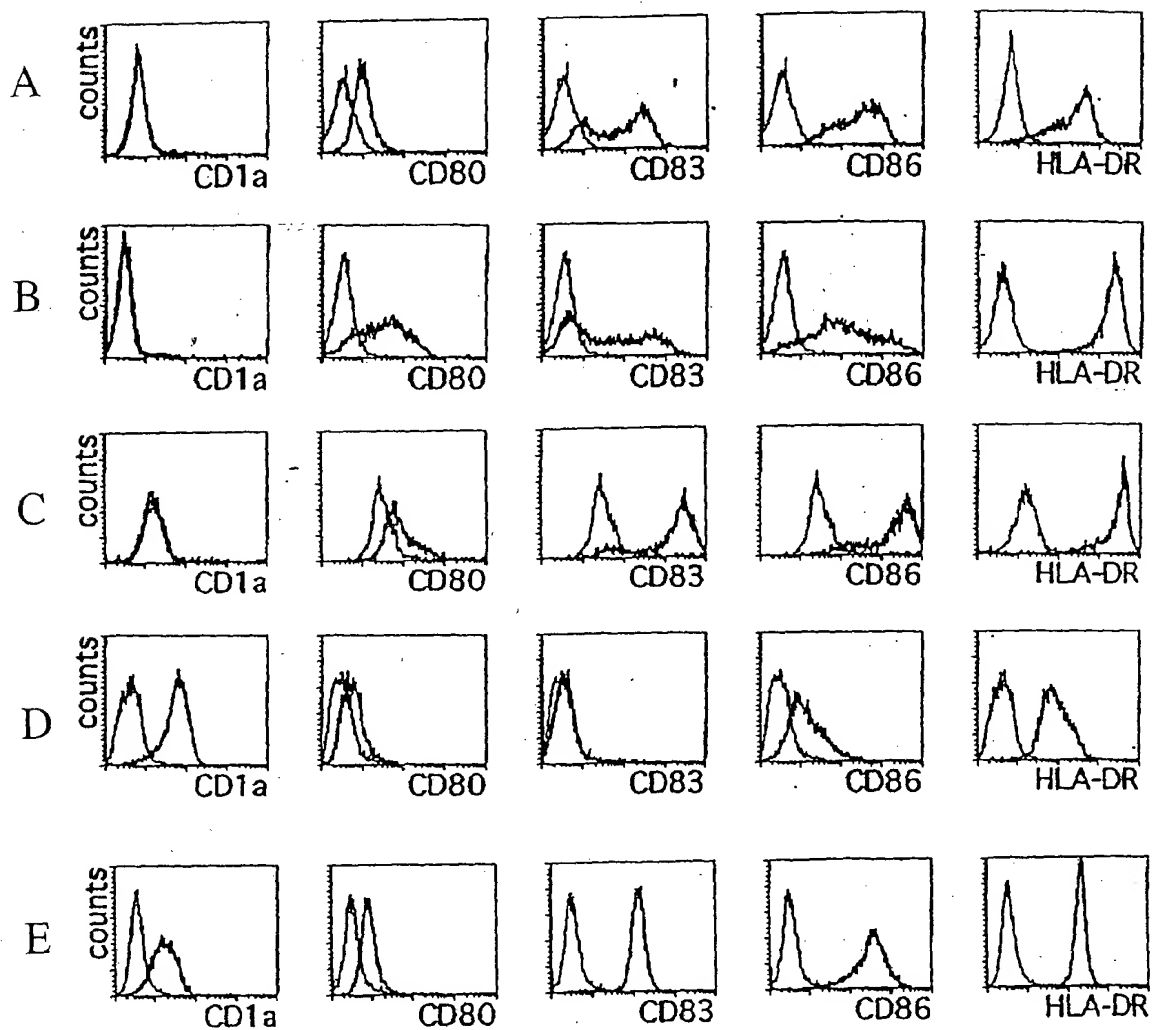


FIGURE 11

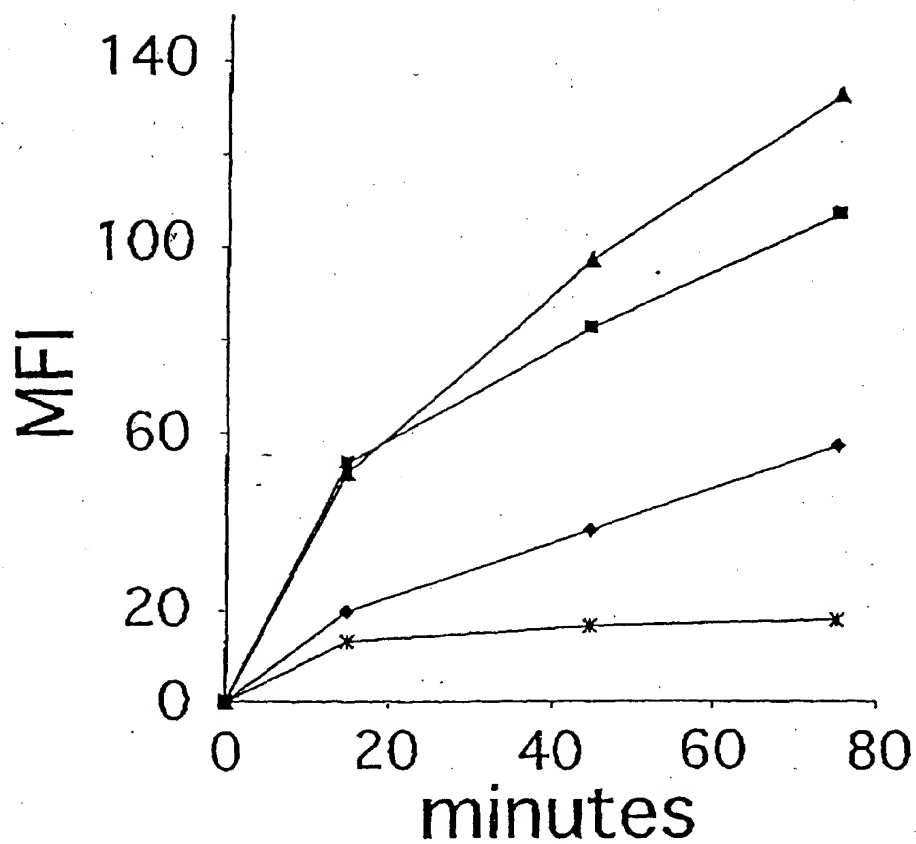


FIGURE 12

CAGTGATTCTCGTGCCTCAGCCTCCTGAGTAGCCGAAATTACAGACGTG
TGCCACCATGCTTGGCTAATTTTTTGGATTTTATAGTAGAGATGGGGTTTC
ACTATGTTGGCCAGGCTAGTCTTGAACCTCCTGGCCTGAAGCAATCCGCC
CACCTCAGCCTCCCAAAGTGCTGAGATTATAGGCACGAGCCACTACAC
CTGGCCACAAAATTCTTTAAAGAAGCCAATCCCATCCTCCCTCAAGAGC
CAAGGGGCCACCTCACCTCTTGTTACAGCAGATCCTGCCTCCACAGTC
ACCCTGCTCCCAAGTGCAACCTCTGTCTGACCCTGCATGGTGTGCGGTG
CCCTCCTGCCTCAGGCCGCGAAGAAGGATCTAAGGGCTTGGCTTGTTTG
AAAGAACCACACCCCGAAAGTAACATCTTTGGAGAAAGTGATACAAGA
GCTTCTGCACCCACCTGATAGAGGAAGTCCAAAGGGTGTGCGCACACA
CAATGGTGCCTGAAGAAGAGCCTCAAGACCGAGAGAAAGGACTCTGGT
GGTTCCAGTTGAAGGTCTGGTCCATGGCAGTCGTATCCATCTTGCTCCT
CAGTGTCTGTTTCACTGTGAGTTCTGTGGTGCCTCACAATTTTATGTATA
GCAAACTGTCAAGAGGCTGTCCAAGTTACGAGAGTATCAACAGTATC
ATCCAAGCCTGACCTGCGTCATGGAAGGAAAGGACATAGAAGATTGGA
GCTGCTGCCCAACCCCTTGGACTTCATTTCACTAGTTGCTACTTTATT
TCTACTGGGATGCAATCTTGGACTAAGAGTCAAAAGAACTGTTCTGTGA
TGGGGGCTGATCTGGTGGTGTGATCAACACCAGGGAAGAACAGGATTTCA
TCATTCAGAATCTGAAAAGAAATTCTTCTTATTTTCTGGGGCTGTCAGA
TCCAGGGGGGTCGGCGACATTGGCAATGGGTTGACCAGACACCATACAA
TGAAAATGTCACATTCTGGCACTCAGGTGAACCCAATAACCTTGATGA
GCGTTGTGCGATAATAAATTTCCGTTCTTCAGAAGAATGGGGCTGGAAT
GACATTCACCTGTCATGTACCTCAGAAGTCAATTTGCAAGATGAAGAAG
ATCTACATATAAATGAAATATTCTCCCTGGAAATGTGTTTGGGTTGGCA
TCCACCGTTGTAGAAAGCTAAATTGATTTTTTAATTTATGTGTAAGTTTT
GTACAAGGAATGCCCCTAAAATGTTTCAGCAGGCTGTCACCTATTACAC
TTATGATATAATCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
(SEQ ID NO:1)



FIGURE 13

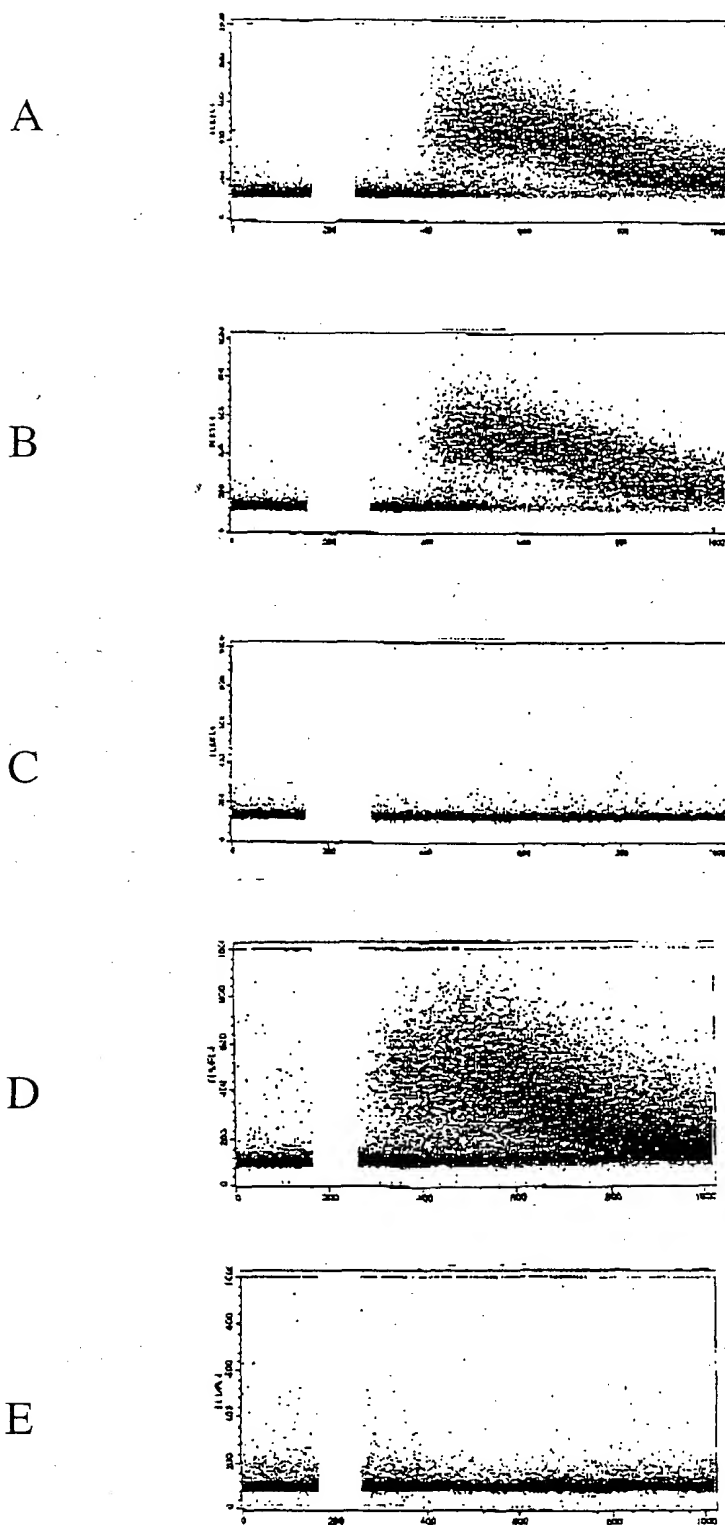
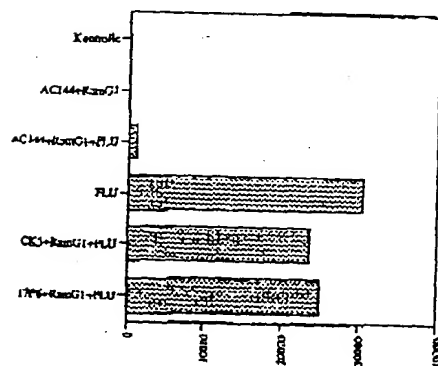


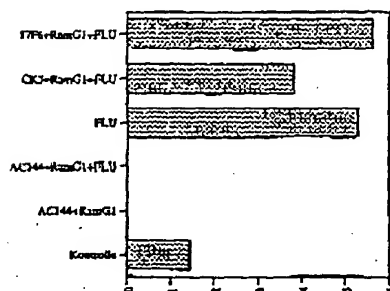
FIGURE 14

A



Type I interferon

B



Type I interferon

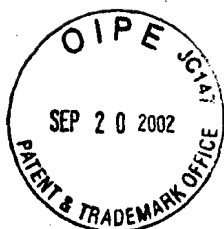


FIGURE 15

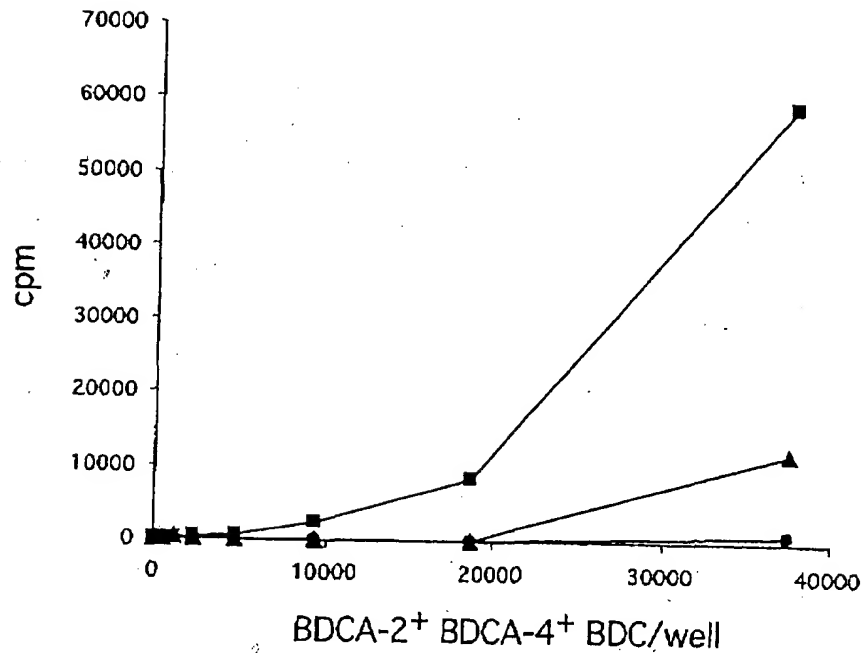


FIGURE 16

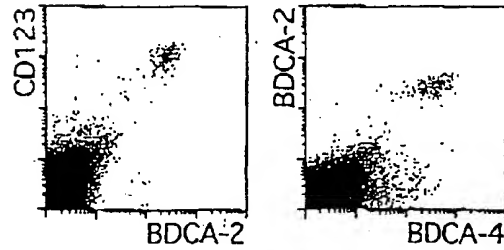


FIGURE 17

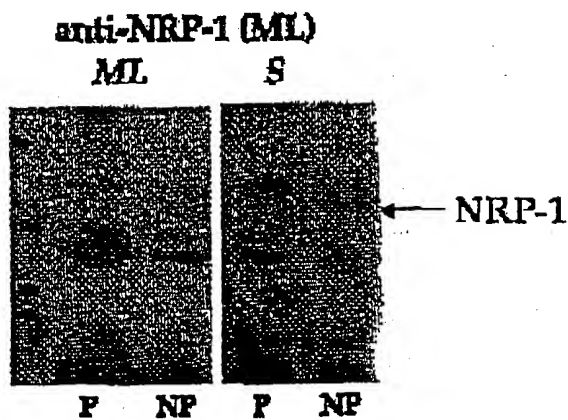


FIGURE 18

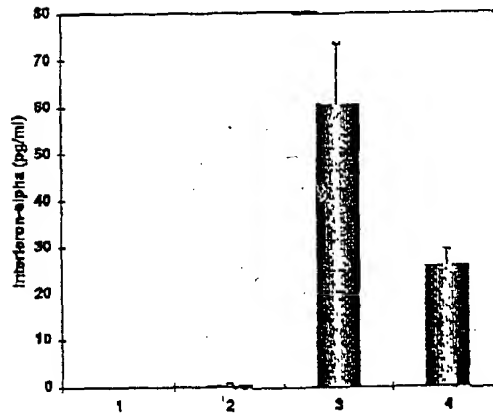
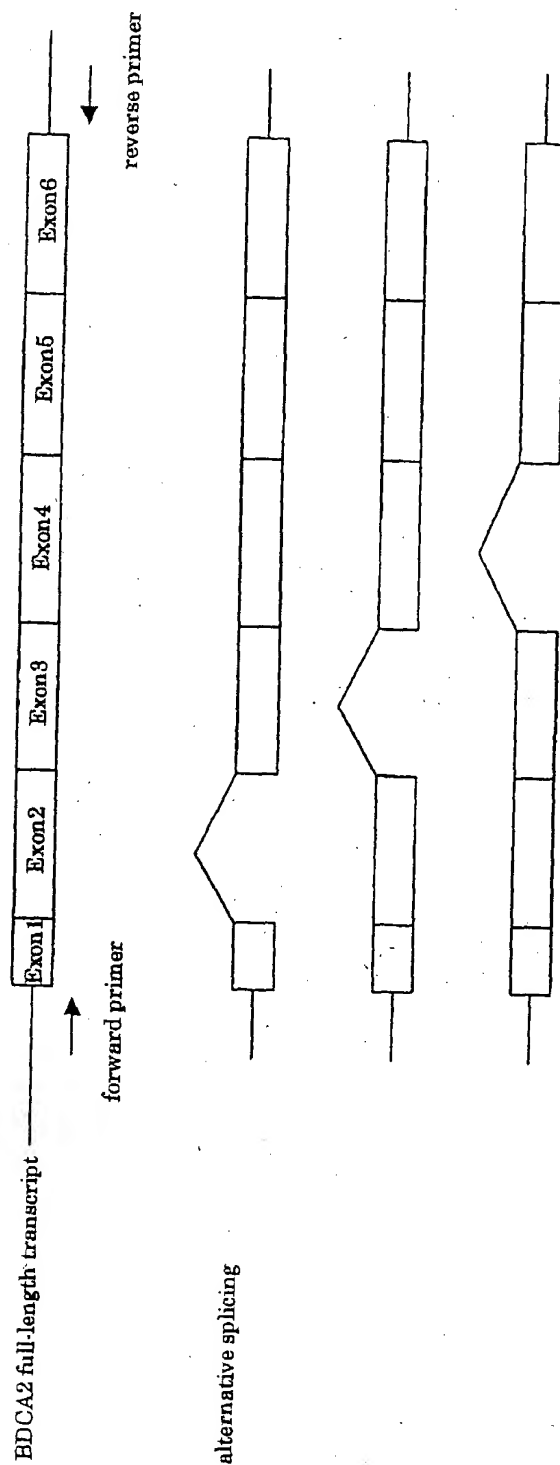


FIGURE 19

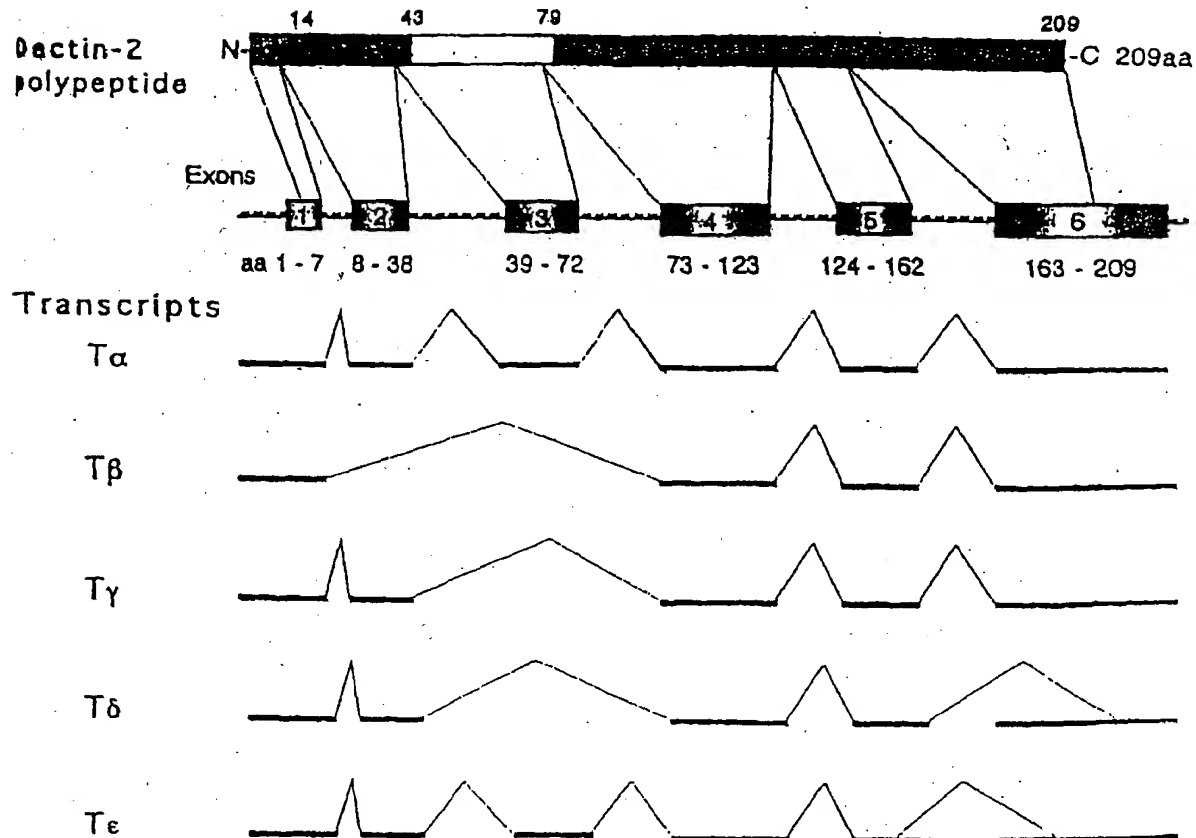


FIGURE 20



sl0357

FIGURE 21



1 mDectin2alph

360 370 380 390 400 410
BDCA2cDNA. tx CCTCAGGCGCGAAGGAAGGATCTAAAGGCTTGGCTTGTGTGGAAGAACACACCCCGAA-
mDectin2alph CATTTGGCCCGCTCTGTGGCATTTAA----CTCAAGTGTGTG-TGGAAGTTGATTTCTGAAC
10 20 30 40 50
BDCA2cDNA. tx AGTAACACTCTTTG-GAGAA-AGTGATCAAGAAG----CTTCTGCACCCCACTGATAGAGG
mDectin2alph TCTGGCCTCTTTGACAGAAGCCAGTCCCTAGTGTGATTTTGGAGACAGATGCAAGA--
60 70 80 90 100 110
BDCA2cDNA. tx AAGTCCAAAGGGTGTGGCGACACACATGTGCTGCTGAAGAAGAGCTCAAGACCGGAGAGA
mDectin2alph AACCCCTGACCTTCTGAACATACACCTCAACATGTGTGCAGGAAGAACAATCCAAAGGGA
120 130 140 150 160 170
BDCA2cDNA. tx AAGGACTCTGCTGTCTCCAGTTCAAGGTCTGGTTCATGGCAGTGGCATTCATCTTGCTGCC
mDectin2alph AGGGAGTCTGCTGGACCTG--AGACTCTGTGTCAGCTGCTGTGATTTTCCATGTTACTCT
180 190 200 210 220 230
BDCA2cDNA. tx TCAGTGTCTGTTTCACTGTGAGTCTCTGTGGCTTCACAATTTATGTATAGCAAAACTG
mDectin2alph TGAATACCTGTTTCAITGCGAGCTGTGTGGTGACTTACCAATTAT-TAT--GGACCAG
240 250 260 270 280
BDCA2cDNA. tx TCAGGAGGCTGTCCAAGTTACGAGAGTATCAACAGTATCATCAAGCCGTGACCTGGCTCA
mDectin2alph CCCAGTAGAAG--ACTATATGA-ACT-TCACACATACCATTCCAGTCTCACTGGCTTCA
290 300 310 320 330 340
BDCA2cDNA. tx -TGGAAGGA--AAGG--ACATAGAAGAT-TGGAGCTGCTGCCAACCCCTTGGACTTTCAT
mDectin2alph GTGAAGGAGACTATGGTGTGAGAAAATATGGGGAGTCTGCCCAAATCATCTGAAGTTCAT
350 360 370 380 390 400
BDCA2cDNA. tx TTCAGTCTAGTTGCTACTTATTTCTACTGGGATGCAATCTTGACTAAGAGTCAAAAAGA
mDectin2alph TTGGCTCCAGCTGCTACTCTATTCTTACCAAGGAGAACTTCTGGAGCAACAGTGAAGAGA
410 420 430 440 450 460
BDCA2cDNA. tx ACTGTTCTGTGATGGGGGCTGATCTGGTGGTGTATCAACACAGGGAAGAACAAGATTCA
mDectin2alph ACTGTGTTTCAGATGGGGGCTCATCTGGTGGTGTATCAATCTGAAGCGGAGCAAAATTCA
470 480 490 500 510 520
BDCA2cDNA. tx TCATTTCAGAAATCTGAA-AAGAAATCTTCTTATTTTCTGGGGCTGTGAGATCCAGGGGT
mDectin2alph TCACCCGACAGCTGAATGAGTCACT-TTCTTACTTCTGGGCTTTTCGGATCCACAAGGT
530 540 550 560 570 580
BDCA2cDNA. tx CGGCGACATTGGCAATGGGTGACGACACCATACAATGAAATGTCACATTCTGGCAC
mDectin2alph AATGGCAAAATGGCAATGGATCGATGATCTCTTTCAGTCAAAAATGTCAGTTCTGGCAC
590 600 610 620 630 640
BDCA2cDNA. tx TCAGGTGAACCAATTAACCTTGATGAGCGTGTGGGTAATAAAATTCGGTCTCTGAGAA
mDectin2alph CCCCATGAACCCAATCTTCCAGAAGAGCGGTGTGTTCAATAGTTTACTTGAATCTCTTCG
650 660 670 680 690 700
BDCA2cDNA. tx GAATGGGGCTGGAATGACATTCACCTGTCATGTACCTCAGAAGTCAATTTCGAAGATGAAG
mDectin2alph AAATGGGGCTGGAATGATGTTTCTGTGTATAGTAACACAATTCATATGTGAAATGAAG
710 720 730 740 750 760
BDCA2cDNA. tx AAGATTACATATTAATGAATAATCTTCCCTGGAAATGTGTGGGTGGCAATCCACCGT
mDectin2alph AAGATTACCTTGTG-TG-CCGTGTATTCATTAATATCT-TTAAAGTTCAGACCTTACC--
770 780 790 800 810
BDCA2cDNA. tx TGTAGAAAGCTAAATGATTTTTTAATTTATGTGTAG-TTTTGTACAGGAAT-GCCCC
mDectin2alph --AAGAAGCCATAACTTCTTGGCCGTGTACATCTGACAGAGGCCGTCTTTTCTAGGCCAC
820 830 840 850 860 870
BDCA2cDNA. tx TAAAAATGT--TTTCAGAGCGTGTACCTATTACCTTATGATATATCAAAAAA
mDectin2alph TATTTCTTACTTCAACAGCAATGAGCCCT-TTCTCTCTGTGTTAGATTTTGTCAAC
880 890 900 910 920 930
BDCA2cDNA. tx AAAAAA (Seq ID No:1)
mDectin2alph TTGACACAATCAGAGTCA (Seq ID No:3)
940 950



FIGURE 23

SEQ ID
NC

BDCA-2	2	MVPEEPQDR--EKGLWWEQLKVWSMAV-----VSILLLSVQFTVS	39
DECTIN-2	4	MVQERQSOG---KGVCT-LRLWSAAV-----ISMILLSTCFIAS	36
DCIR	5	MTSEITYAEVRFKNEFKSSGINTASSAASKERTAPHKSENTGFPKLLCASLIIFFLLAIS	60
		*. * : . : . * . * : * : : *	
BDCA-2		SWPHNFMYSKTVKRLSKLREYQQYHPSLTCVMEGKDIED--WSC	97
DECTIN-2		CVVTYQFIMDQPSRRLYEL---HTYRSSLTCFSEGTMVSEKMWGC	93
DCIR		FFIAFVIFPQKYSQLEKKTTELKLVHTTLECVKKNMPVEETAWSCH	120
	 : : : * : . * : * * : . : : * * * . * * * * : *	
BDCA-2		Δ A C A A E HA ΔAGA + Δ H	157
DECTIN-2			153
DCIR			180
		** * : : * * * : * * : * : * : * : * : * : * : * : * : *	
BDCA-2		H W +P++ ++CA W++ C C	213
DECTIN-2			209
DCIR			237
		* : : . * * . * : * : : . . . * : * : * : * : * : *	



FIGURE 24

